ORF2558c (SEQ ID NO:24), ORF2929c (SEQ ID NO:26), ORF3965c (SEQ ID NO:28), ORF3218 (SEQ ID NO:30), ORF3568 (SEQ ID NO:32), ORF4506c (SEQ ID NO:34), ORF3973 (SEQ ID NO:36), ORF4271 (SEQ ID NO:38), ORF4698 (SEQ ID NO:40), ORF5028 (SEQ ID NO:42), ORF5080 (SEQ ID NO:44), ORF6479c (SEQ ID NO:46), ORF5496 (SEQ ID NO:48), ORF5840 (SEQ ID NO:50), ORF5899 (SEQ ID NO:52), ORF6325 (SEQ ID NO:54), ORF7567c (SEQ ID NO:56), ORF7180 (SEQ ID NO:58), ORF7501 (SEQ ID NO:60), ORF7584 (SEQ ID NO:62), ORF8208c (SEQ ID NO:64), ORF8109 (SEQ ID NO:66), ORF9005c (SEQ ID NO:68), ORF8222 (SEQ ID NO:70), ORF8755c (SEQ ID NO:72), ORF9431c (SEQ ID NO:74), ORF9158 (SEQ ID NO:76), ORF10125c (SEQ ID NO:78), ORF9770 (SEQ ID NO:80), ORF9991 (SEQ ID NO:82), ORF10765c (SEQ ID NO:84), ORF10475 (SEQ ID NO:86), ORF11095c (SEQ ID NO:88), ORF11264 (SEQ ID NO:90), ORF11738 (SEQ ID NO:92), ORF12348c (SEQ ID NO:94), ORF12314c (SEQ ID NO:96), ORF13156c (SEQ ID NO:98), ORF12795 (SEQ ID NO:100), ORF13755c (SEQ ID NO:210), ORF13795c (SEQ ID NO:212), ORF14727c (SEQ ID NO:214), ORF13779 (SEQ ID NO:216), ORF14293c (SEQ ID NO:218), ORF14155 (SEQ ID NO:220), ORF14360 (SEQ ID NO:222), ORF15342c (SEQ ID NO:224), ORF15260c (SEQ ID NO:226), ORF14991 (SEQ ID NO:228), ORF15590c (SEQ ID NO:230), ORF15675c (SEQ ID NO:232), ORF16405 (SEQ ID NO:234), ORF16925 (SEQ ID NO:236), ORF17793c (SEQ ID NO:238), ORF18548c (SEQ ID NO:240), ORF17875 (SEQ ID NO:242), ORF18479 (SEQ ID NO:244), ORF19027c (SEQ ID NO:246), ORF19305 (SEQ ID NO:248), ORF19519 (SEQ ID NO:250), ORF19544 (SEQ ID NO:252), ORF20008 (SEQ ID NO:254), ORF20623c (SEQ ID NO:256), ORF21210c (SEQ ID NO:258), ORF21493c (SEQ ID NO:260), ORF21333 (SEQ ID NO:262), ORF22074c (SEQ ID NO:264), ORF21421 (SEQ ID NO:266), ORF22608c (SEQ ID NO:268), ORF22626 (SEQ ID NO:270), ORF23228 (SEQ ID NO:272),ORF23367 (SEQ ID NO:274), ORF25103c (SEQ ID NO:276), ORF23556 (SEQ ID NO:278), ORF26191c (SEQ ID NO:280), ORF23751 (SEQ ID NO:282), ORF24222 (SEQ ID NO:284), ORF24368 (SEQ ID NO:286), ORF24888c (SEQ ID NO:288), ORF25398c (SEQ ID NO:290), ORF25892c (SEQ ID NO:292), ORF25110 (SEQ ID NO:294), ORF25510 (SEQ ID NO:296), ORF26762c (SEQ ID NO:298), ORF26257 (SEQ ID NO:300), ORF26844c (SEQ ID NO:302), ORF26486 (SEQ ID NO:304), ORF26857c (SEQ ID NO:306), ORF27314c (SEQ ID NO:308), ORF27730c (SEQ ID NO:310), ORF26983 (SEQ ID NO:312), ORF28068c (SEQ ID NO:314), ORF27522 (SEQ ID NO:316), ORF28033c (SEQ ID NO:318), ORF29701c (SEQ ID NO:320), ORF28118 (SEQ ID NO:322), ORF28129 (SEQ ID NO:324), ORF29709c (SEQ ID NO:326), ORF29189 (SEQ ID NO:328), ORF29382 (SEQ ID NO:330), ORF30590c (SEQ ID NO:332), ORF29729 (SEQ

ID NO:334), ORF30221 (SEQ ID NO:336), ORF30736c (SEQ ID NO:338), ORF30539 (SEQ ID NO:340), ORF31247c (SEQ ID NO:342), ORF30963c (SEQ ID NO: 344), ORF31539c (SEQ ID NO:346), ORF31222 (SEQ ID NO:348), ORF31266 (SEQ ID NO:350), ORF31661c (SEQ ID NO:352), ORF32061c (SEQ ID NO:354), ORF32072c (SEQ ID NO:356), ORF31784 (SEQ ID NO:358), ORF32568c (SEQ ID NO:360), ORF33157c (SEQ ID NO:362), ORF32530 (SEQ ID NO:364), ORF33705c (SEQ ID NO:366), ORF32832 (SEQ ID NO:368), ORF33547c (SEQ ID NO:370), ORF33205 (SEQ ID NO:372), ORF33512 (SEQ ID NO:374), ORF33771 (SEQ ID NO:376), ORF34385c (SEQ ID NO:378), ORF33988 (SEQ ID NO:380), ORF34274 (SEQ ID NO:382), ORF34726c (SEQ ID NO:384), ORF34916 (SEQ ID NO:386), ORF35464c (SEQ ID NO:388), ORF35289 (SEQ ID NO:390), ORF35410 (SEQ ID NO:392), ORF35907c (SEQ ID NO:394),ORF35534 (SEQ ID NO:396), ORF35930 (SEQ ID NO:398), ORF36246 (SEQ ID NO:400), ORF26640c (SEQ ID NO:402), ORF36769 (SEQ ID NO:404), ORF37932c (SEQ ID NO:406), ORF38640c (SEQ ID NO:408), ORF39309c (SEQ ID NO:410), ORF38768 (SEQ ID NO:412), ORF40047c (SEQ ID NO:414), ORF40560c (SEQ ID NO:416), ORF40238 (SEQ ID NO:418), ORF40329 (SEQ ID NO:420), ORF40709c (SEQ ID NO:422), ORF40507 (SEQ ID NO:424), ORF41275c (SEQ ID NO:426), ORF42234c (SEQ ID NO:428), ORF41764c (SEQ ID NO:430), ORF41284 (SEQ ID NO:432), ORF41598 (SEQ ID NO:434), ORF42172c (SEQ ID NO:436), ORF42233c (SEQ ID NO:151), 33A9 (SEQ ID NO:102, 189, 190, 191, 192, 193, 194, 195, 196, 197, and 198), *34B12* (SEQ ID NO:104), *34B12-ORF1* (SEQ ID NO:105), *34B12-ORF2* (SEQ ID NO:106), *36A4* (SEQ ID NO:109), *36A4 contig* (SEQ ID NO:111), *23A2* (SEQ ID NO:112), *3E8 phn(-)*(SEQ ID NO:114), *3E8 contigPAO1* (SEQ ID NO:115), *34H4* (SEQ ID NO:118), *33C7* (SEQ ID NO:119), *25a12.3* (SEQ ID NO:120), *8C12* (SEQ ID NO:121), *2A8* (SEQ ID NO:122), *41A5* (SEQ ID NO:123), *50E12* (SEQ ID NO:124), *35A9* (SEQ ID NO:125), *pho23* (SEQ ID NO:126), *16G12* (SEQ ID NO:127), *25F1* (SEQ ID NO:128), *PA14 degP* (SEQ ID NO:131), 1126 contig (SEQ ID NO:135), contig 1344 (SEQ ID NO:136), ORFA (SEQ ID NO:153), ORFB (SEQ ID NO:154), ORFC (SEQ ID NO:155), *phzR* (SEQ ID NO:164, and 1G2 (SEQ ID NO:137). Preferably, the isolated nucleic acid molecule includes any of the above-described sequences or a fragment thereof; and is derived from a pathogen (e.g., from a bacterial pathogen such as *Pseudomonas aeruginosa*). Additionally, the invention includes a vector and a cell, each of which includes at least one of the isolated nucleic acid molecules of the invention; and a method of producing a recombinant polypeptide involving providing a cell transformed with a nucleic acid molecule of the invention positioned for expression in the cell, culturing the transformed cell under conditions for expressing the nucleic acid molecule, and isolating a

recombinant polypeptide. The invention further features recombinant polypeptides produced by such expression of an isolated nucleic acid molecule of the invention, and substantially pure antibodies that specifically recognize and bind such a recombinant polypeptides.

Replace the paragraph on page 5, line 22 through page 8, line 9 of the specification with the following paragraph that has been re-written in clean form.

In an another aspect, the invention features a substantially pure polypeptide including an amino acid sequence that is substantially identical to the amino acid sequence of any one of ORF2 (SEQ ID NO:3), ORF3 (SEQ ID NO:5), ORF602c (SEQ ID NO:7), ORF214 (SEQ ID NO:9),ORF1242c (SEQ ID NO:11), ORF594 (SEQ ID NO:13), ORF1040 (SEQ ID NO:15), ORF1640c (SEQ ID NO:17), ORF2228c (SEQ ID NO:19), ORF2068c (SEQ ID NO:21), ORF1997 (SEQ ID NO:23), ORF2558c (SEQ ID NO:25), ORF2929c (SEQ ID NO:27), ORF3965c (SEQ ID NO:29), ORF3218 (SEQ ID NO:31), ORF3568 (SEQ ID NO:33), ORF4506c (SEQ ID NO:35), ORF3973 (SEQ ID NO:37), ORF4271 (SEQ ID NO:39), ORF4698 (SEQ ID NO:41), ORF5028 (SEQ ID NO:43), ORF5080 (SEQ ID NO:45), ORF6479c (SEQ ID NO:47), ORF5496 (SEQ ID NO:49), ORF5840 (SEQ ID NO:51), ORF5899 (SEQ ID NO:53), ORF6325 (SEQ ID NO:55), ORF7567c (SEQ ID NO:57), ORF7180 (SEQ ID NO:59), ORF7501 (SEQ ID NO:61), ORF7584 (SEQ ID NO:63), ORF8208c (SEQ ID NO:65), ORF8109 (SEQ ID NO:67), ORF9005c (SEQ ID NO:69), ORF8222 (SEQ ID NO:71), ORF8755c (SEQ ID NO:73), ORF9431c (SEQ ID NO:75), ORF9158 (SEQ ID NO:77), ORF10125c (SEQ ID NO:79), ORF9770 (SEQ ID NO:81), ORF9991 (SEQ ID NO:83), ORF10765c (SEQ ID NO:85), ORF10475 (SEQ ID NO:87), ORF11095c (SEQ ID NO:89), ORF11264 (SEQ ID NO:91), ORF11738 (SEQ ID NO:93), ORF12348c (SEQ ID NO:95), ORF12314c (SEQ ID NO:97), ORF13156c (SEQ ID NO:99), ORF12795 (SEQ ID NO:101), ORF13755c (SEQ ID NO:211), ORF13795c (SEQ ID NO:213), ORF14727c (SEQ ID NO:215), ORF13779 (SEQ ID NO:217), ORF14293c (SEQ ID NO:219), ORF14155 (SEQ ID NO:221), ORF14360 (SEQ ID NO:223), ORF15342c (SEQ ID NO:225), ORF15260c (SEQ ID NO:227), ORF14991 (SEQ ID NO:229), ORF15590c (SEQ ID NO:231), ORF15675c (SEQ ID NO:233), ORF16405 (SEQ ID NO:235), ORF16925 (SEQ ID NO:237), ORF17793c (SEQ ID NO:239), ORF18548c (SEQ ID NO:241), ORF17875 (SEQ ID NO:243), ORF18479 (SEQ ID NO:245), ORF19027c (SEQ ID NO:247), ORF19305 (SEQ ID NO:249), ORF19519 (SEQ ID NO:251), ORF19544 (SEQ ID NO:253), ORF20008 (SEQ ID NO:255), ORF20623c (SEQ ID NO:257), ORF21210c (SEQ ID NO:259), ORF21493c

(SEQ ID NO:261), ORF21333 (SEQ ID NO:263), ORF22074c (SEQ ID NO:265), ORF21421 (SEQ ID NO:267), ORF22608c (SEQ ID NO:269), ORF22626 (SEQ ID NO:271), ORF23228 (SEQ ID NO:273), ORF23367 (SEQ ID NO:275), ORF25103c (SEQ ID NO:277), ORF23556 (SEQ ID NO:279), ORF26191c (SEQ ID NO:281), ORF23751 (SEQ ID NO:283), ORF24222 (SEQ ID NO:285), ORF24368 (SEQ ID NO:287), ORF24888c (SEQ ID NO:289), ORF25398c (SEQ ID NO:291), ORF25892c (SEQ ID NO:293), ORF25110 (SEQ ID NO:295), ORF25510 (SEQ ID NO:297), ORF26762c (SEQ ID NO:299), ORF26257 (SEQ ID NO:301), ORF26844c (SEQ ID NO:303), ORF26486 (SEQ ID NO:305), ORF26857c (SEQ ID NO:307), ORF27314c (SEQ ID NO:309), ORF27730c (SEQ ID NO:311), ORF26983 (SEQ ID NO:313), ORF28068c (SEQ ID NO:315), ORF27522 (SEQ ID NO:317), ORF28033c (SEQ ID NO:319), ORF29701c (SEQ ID NO:321), ORF28118 (SEQ ID NO:323), ORF28129 (SEQ ID NO:325), ORF29709c (SEQ ID NO:327), ORF29189 (SEQ ID NO:329), ORF29382 (SEQ ID NO:331), ORF30590c (SEQ ID NO:333), ORF29729 (SEQ ID NO:335), ORF30221 (SEQ ID NO:337), ORF30736c (SEQ ID NO:339), ORF30539 (SEQ ID NO:341), ORF31247c (SEQ ID NO:343), ORF30963c (SEQ ID NO:345), ORF31539c (SEQ ID NO:347), ORF31222 (SEQ ID NO:349), ORF31266 (SEQ ID NO:351), ORF31661c (SEQ ID NO:353), ORF32061c (SEQ ID NO:355), ORF32072c (SEQ ID NO:357), ORF31784 (SEQ ID NO:359), ORF32568c (SEQ ID NO:361), ORF33157c (SEQ ID NO:363), ORF32530 (SEQ ID NO:365), ORF33705c (SEQ ID NO:367), ORF32832 (SEQ ID NO:369), ORF33547c (SEQ ID NO:371), ORF33205 (SEQ ID NO:373), ORF33512 (SEQ ID NO:375), ORF33771 (SEQ ID NO:377), ORF34385c (SEQ ID NO:379), ORF33988 (SEQ ID NO:381), ORF34274 (SEQ ID NO:383), ORF34726c (SEQ ID NO:385), ORF34916 (SEQ ID NO:387), ORF35464c (SEQ ID NO:389), ORF35289 (SEQ ID NO:391), ORF35410 (SEQ ID NO:393), ORF35907c (SEQ ID NO:395), ORF35534 (SEQ ID NO:397), ORF35930 (SEQ ID NO:399), ORF36246 (SEQ ID NO:401), ORF26640c (SEQ ID NO:403), ORF36769 (SEQ ID NO:405), ORF37932c (SEQ ID NO:407), ORF38640c (SEQ ID NO:409), ORF39309c (SEQ ID NO:411), ORF38768 (SEQ ID NO:413), ORF40047c (SEQ ID NO:415), ORF40560c (SEQ ID NO:417), ORF40238 (SEQ ID NO:419), ORF40329 (SEQ ID NO:421), ORF40709c (SEQ ID NO:423), ORF40507 (SEQ ID NO:425), ORF41275c (SEQ ID NO:427), ORF42234c (SEQ ID NO:429), ORF41764c (SEQ ID NO:431), ORF41284 (SEQ ID NO:433), ORF41598 (SEQ ID NO:435), ORF42172c (SEQ ID NO:437), ORF42233c (SEQ ID NO:152), *33A9* (SEQ ID NOS:103, 199, 200, 201, 202, 203, 204, 205, 206, 207, and 208), *34B12-ORF1* (SEQ ID NO:107), *34B12-ORF2* (SEQ ID NO:108), *36A4* (SEQ ID NO:110), *3E8phzA* (SEQ ID NO:116), *3E8phzB* (SEQ ID NO:117), PhzR (SEQ ID NO:165), ORFA (SEQ ID NO:156), ORFB (SEQ ID NO:157), ORFC (SEQ

ID NO:158), and *PA14 degP* (SEQ ID NO:132). Preferably, the substantially pure polypeptide includes any of the above-described sequences of a fragment thereof; and is derived from a pathogen (e.g., from a bacterial pathogen such as *Pseudomonas aeruginosa*).

Please replace the paragraph on page 13, lines 1 and 2, with the following paragraph that has been re-written in clean form.

Figs. 1A-1C are schematic diagrams showing the physical map of cosmid BI48 (SEQ ID NO:1) and the orientation of the identified open reading frames (ORFs).

Please replace the paragraph on page 13, line 3 of the specification with the following paragraph that has been re-written in clean form.

Figs. 2A-2K show the nucleotide sequence of cosmid BI48 (SEQ ID NO:1).

Please replace the paragraph on page 13, line 4 through page 15, line 10 with the following paragraph that has been re-written in clean form.

Figs. 3-1 to 3-39 show the nucleotide sequences for ORF2 (SEQ ID NO:2), ORF3 (SEQ ID NO:4), ORF602c (SEQ ID NO:6), ORF214 (SEQ ID NO:8), ORF1242c (SEQ ID NO:10), ORF594 (SEQ ID NO:12), ORF1040 (SEQ ID NO:14), ORF1640c (SEQ ID NO:16), ORF2228c (SEQ ID NO:18), ORF2068c (SEQ ID NO:20), ORF1997 (SEQ ID NO:22), ORF2558c (SEQ ID NO:24), ORF2929c (SEQ ID NO:26), ORF3965c (SEQ ID NO:28), ORF3218 (SEQ ID NO:30), ORF3568 (SEQ ID NO:32), ORF4506c (SEQ ID NO:34), ORF3973 (SEQ ID NO:36), ORF4271 (SEQ ID NO:38), ORF4698 (SEQ ID NO:40), ORF5028 (SEQ ID NO:42), ORF5080 (SEQ ID NO:44), ORF6479c (SEQ ID NO:46), ORF5496 (SEQ ID NO:48), ORF5840 (SEQ ID NO:50), ORF5899 (SEQ ID NO:52), ORF6325 (SEQ ID NO:54), ORF7567c (SEQ ID NO:56), ORF7180 (SEQ ID NO:58), ORF7501 (SEQ ID NO:60), ORF7584 (SEQ ID NO:62), ORF8208c (SEQ ID NO:64), ORF8109 (SEQ ID NO:66), ORF9005c (SEQ ID NO:68), ORF8222 (SEQ ID NO:70), ORF8755c (SEQ ID

NO:72), ORF9431c (SEQ ID NO:74), ORF9158 (SEQ ID NO:76), ORF10125c (SEQ ID NO:78), ORF9770 (SEQ ID NO:80), ORF9991 (SEQ ID NO:82), ORF10765c (SEQ ID NO:84), ORF10475 (SEQ ID NO:86), ORF11095c (SEQ ID NO:88), ORF11264 (SEQ ID NO:90), ORF11738 (SEQ ID NO:92), ORF12348c (SEQ ID NO:94), ORF12314c (SEQ ID NO:96), ORF13156c (SEQ ID NO:98), ORF12795 (SEQ ID NO:100), ORF13755c (SEQ ID NO:210), ORF13795c (SEQ ID NO:212), ORF14727c (SEQ ID NO:214), ORF13779 (SEQ ID NO:216), ORF14293c (SEQ ID NO:218), ORF14155 (SEQ ID NO:220), ORF14360 (SEQ ID NO:222), ORF15342c (SEQ ID NO:224), ORF15260c (SEQ ID NO:226), ORF14991 (SEQ ID NO:228), ORF15590c (SEQ ID NO:230), ORF15675c (SEQ ID NO:232), ORF16405 (SEQ ID NO:234), ORF16925 (SEQ ID NO:236), ORF17793c (SEQ ID NO:238), ORF18548c (SEQ ID NO:240), ORF17875 (SEQ ID NO:242), ORF18479 (SEQ ID NO:244), ORF19027c (SEQ ID NO:246), ORF19305 (SEQ ID NO:248), ORF19519 (SEQ ID NO:250), ORF19544 (SEQ ID NO:252), ORF20008 (SEQ ID NO:254), ORF20623c (SEQ ID NO:256), ORF21210c (SEQ ID NO:258), ORF21493c (SEQ ID NO:260), ORF21333 (SEQ ID NO:262), ORF22074c (SEQ ID NO:264), ORF21421 (SEQ ID NO:266), ORF22608c (SEQ ID NO:268), ORF22626 (SEQ ID NO:270), ORF23228 (SEQ ID NO:272),ORF23367 (SEQ ID NO:274), ORF25103c (SEQ ID NO:276), ORF23556 (SEQ ID NO:278), ORF26191c (SEQ ID NO:280), ORF23751 (SEQ ID NO:282), ORF24222 (SEQ ID NO:284), ORF24368 (SEQ ID NO:286), ORF24888c (SEQ ID NO:288), ORF25398c (SEQ ID NO:290), ORF25892c (SEQ ID NO:292), ORF25110 (SEQ ID NO:294), ORF25510 (SEQ ID NO:296), ORF26762c (SEQ ID NO:298), ORF26257 (SEQ ID NO:300), ORF26844c (SEQ ID NO:302), ORF26486 (SEQ ID NO:304), ORF26857c (SEQ ID NO:306), ORF27314c (SEQ ID NO:308), ORF27730c (SEQ ID NO:310), ORF26983 (SEQ ID NO:312), ORF28068c (SEQ ID NO:314), ORF27522 (SEQ ID NO:316), ORF28033c (SEQ ID NO:318), ORF29701c (SEQ ID NO:320), ORF28118 (SEQ ID NO:322), ORF28129 (SEQ ID NO:324), ORF29709c (SEQ ID NO:326), ORF29189 (SEQ ID NO:328), ORF29382 (SEQ ID NO:330), ORF30590c (SEQ ID NO:332), ORF29729 (SEQ ID NO:334), ORF30221 (SEQ ID NO:336), ORF30736c (SEQ ID NO:338), ORF30539 (SEQ ID NO:340), ORF31247c (SEQ ID NO:342), ORF30963c (SEQ ID NO:344), ORF31539c (SEQ ID NO:346), ORF31222 (SEQ ID NO:348), ORF31266 (SEQ ID NO:350), ORF31661c (SEQ ID NO:352), ORF32061c (SEQ ID NO:354), ORF32072c (SEQ ID NO:356), ORF31784 (SEQ ID NO:358), ORF32568c (SEQ ID NO:360), ORF33157c (SEQ ID NO:362), ORF32530 (SEQ ID NO:364), ORF33705c (SEQ ID NO:366), ORF32832 (SEQ ID NO:368), ORF33547c (SEQ ID NO:370), ORF33205 (SEQ ID NO:372), ORF33512 (SEQ ID NO:374), ORF33771 (SEQ ID NO:376), ORF34385c (SEQ ID NO:378), ORF33988 (SEQ

ID NO:380), ORF34274 (SEQ ID NO:382), ORF34726c (SEQ ID NO:384), ORF34916 (SEQ ID NO:386), ORF35464c (SEQ ID NO:388), ORF35289 (SEQ ID NO:390), ORF35410 (SEQ ID NO:392), ORF35907c (SEQ ID NO:394),ORF35534 (SEQ ID NO:396), ORF35930 (SEQ ID NO:398), ORF36246 (SEQ ID NO:400), ORF26640c (SEQ ID NO:402), ORF36769 (SEQ ID NO:404), ORF37932c (SEQ ID NO:406), ORF38640c (SEQ ID NO:408), ORF39309c (SEQ ID NO:410), ORF38768 (SEQ ID NO:412), ORF40047c (SEQ ID NO:414), ORF40560c (SEQ ID NO:416), ORF40238 (SEQ ID NO:418), ORF40329 (SEQ ID NO:420), ORF40709c (SEQ ID NO:422), ORF40507 (SEQ ID NO:424), ORF41275c (SEQ ID NO:426), ORF42234c (SEQ ID NO:428), ORF41764c (SEQ ID NO:430), ORF41284 (SEQ ID NO:432), ORF41598 (SEQ ID NO:434), ORF42172c (SEQ ID NO:436), and ORF42233c (SEQ ID NO:151).

Replace the paragraph on page 15, line 11 through page 17, line 17 of the specification with the following paragraph that has been re-written in clean form.

Fig. 4 shows the deduced amino acid sequences for ORF2 (SEQ ID NO:3), ORF3 (SEQ ID NO:5), ORF602c (SEQ ID NO:7), ORF214 (SEQ ID NO:9),ORF1242c (SEQ ID NO:11), ORF594 (SEQ ID NO:13), ORF1040 (SEQ ID NO:15), ORF1640c (SEQ ID NO:17), ORF2228c (SEQ ID NO:19), ORF2068c (SEQ ID NO:21), ORF1997 (SEQ ID NO:23), ORF2558c (SEQ ID NO:25), ORF2929c (SEQ ID NO:27), ORF3965c (SEQ ID NO:29), ORF3218 (SEQ ID NO:31), ORF3568 (SEQ ID NO:33), ORF4506c (SEQ ID NO:35), ORF3973 (SEQ ID NO:37), ORF4271 (SEQ ID NO:39), ORF4698 (SEQ ID NO:41), ORF5028 (SEQ ID NO:43), ORF5080 (SEQ ID NO:45), ORF6479c (SEQ ID NO:47), ORF5496 (SEQ ID NO:49), ORF5840 (SEQ ID NO:51), ORF5899 (SEQ ID NO:53), ORF6325 (SEQ ID NO:55), ORF7567c (SEQ ID NO:57), ORF7180 (SEQ ID NO:59), ORF7501 (SEQ ID NO:61), ORF7584 (SEQ ID NO:63), ORF8208c (SEQ ID NO:65), ORF8109 (SEQ ID NO:67), ORF9005c (SEQ ID NO:69), ORF8222 (SEQ ID NO:71), ORF8755c (SEQ ID NO:73), ORF9431c (SEQ ID NO:75), ORF9158 (SEQ ID NO:77), ORF10125c (SEQ ID NO:79), ORF9770 (SEQ ID NO:81), ORF9991 (SEQ ID NO:83), ORF10765c (SEQ ID NO:85), ORF10475 (SEQ ID NO:87), ORF11095c (SEQ ID NO:89), ORF11264 (SEQ ID NO:91), ORF11738 (SEQ ID NO:93), ORF12348c (SEQ ID NO:95), ORF12314c (SEQ ID NO:97), ORF13156c (SEQ ID NO:99), ORF12795 (SEQ ID NO:101), ORF13755c (SEQ ID NO:211), ORF13795c (SEQ ID NO:213), ORF14727c (SEQ ID NO:215), ORF13779 (SEQ ID NO:217), ORF14293c (SEQ ID NO:219), ORF14155 (SEQ ID NO:221), ORF14360 (SEQ ID NO:223), ORF15342c (SEQ ID NO:225), ORF15260c (SEQ

ID NO:227), ORF14991 (SEQ ID NO:229), ORF15590c (SEQ ID NO:231), ORF15675c (SEQ ID NO:233), ORF16405 (SEQ ID NO:235), ORF16925 (SEQ ID NO:237), ORF17793c (SEQ ID NO:239), ORF18548c (SEQ ID NO:241), ORF17875 (SEQ ID NO:243), ORF18479 (SEQ ID NO:245), ORF19027c (SEQ ID NO:247), ORF19305 (SEQ ID NO:249), ORF19519 (SEQ ID NO:251), ORF19544 (SEQ ID NO:253), ORF20008 (SEQ ID NO:255), ORF20623c (SEQ ID NO:257), ORF21210c (SEQ ID NO:259), ORF21493c (SEQ ID NO:261), ORF21333 (SEQ ID NO:263), ORF22074c (SEQ ID NO:265), ORF21421 (SEQ ID NO:267), ORF22608c (SEQ ID NO:269), ORF22626 (SEQ ID NO:271), ORF23228 (SEQ ID NO:273), ORF23367 (SEQ ID NO:275), ORF25103c (SEQ ID NO:277), ORF23556 (SEQ ID NO:279), ORF26191c (SEQ ID NO:281), ORF23751 (SEQ ID NO:283), ORF24222 (SEQ ID NO:285), ORF24368 (SEQ ID NO:287), ORF24888c (SEQ ID NO:289), ORF25398c (SEQ ID NO:291), ORF25892c (SEQ ID NO:293), ORF25110 (SEQ ID NO:295), ORF25510 (SEQ ID NO:297), ORF26762c (SEQ ID NO:299), ORF26257 (SEQ ID NO:301), ORF26844c (SEQ ID NO:303), ORF26486 (SEQ ID NO:305), ORF26857c (SEQ ID NO:307), ORF27314c (SEQ ID NO:309), ORF27730c (SEQ ID NO:311), ORF26983 (SEQ ID NO:313), ORF28068c (SEQ ID NO:315), ORF27522 (SEQ ID NO:317), ORF28033c (SEQ ID NO:319), ORF29701c (SEQ ID NO:321), ORF28118 (SEQ ID NO:323), ORF28129 (SEQ ID NO:325), ORF29709c (SEQ ID NO:327), ORF29189 (SEQ ID NO:329), ORF29382 (SEQ ID NO:331), ORF30590c (SEQ ID NO:333), ORF29729 (SEQ ID NO:335), ORF30221 (SEQ ID NO:337), ORF30736c (SEQ ID NO:339), ORF30539 (SEQ ID NO:341), ORF31247c (SEQ ID NO:343), ORF30963c (SEQ ID NO:345), ORF31539c (SEQ ID NO:347), ORF31222 (SEQ ID NO:349), ORF31266 (SEQ ID NO:351), ORF31661c (SEQ ID NO:353), ORF32061c (SEQ ID NO:355), ORF32072c (SEQ ID NO:357), ORF31784 (SEQ ID NO:359), ORF32568c (SEQ ID NO:361), ORF33157c (SEQ ID NO:363), ORF32530 (SEQ ID NO:365), ORF33705c (SEQ ID NO:367), ORF32832 (SEQ ID NO:369), ORF33547c (SEQ ID NO:371), ORF33205 (SEQ ID NO:373), ORF33512 (SEQ ID NO:375), ORF33771 (SEQ ID NO:377), ORF34385c (SEQ ID NO:379), ORF33988 (SEQ ID NO:381), ORF34274 (SEQ ID NO:383), ORF34726c (SEQ ID NO:385), ORF34916 (SEQ ID NO:387), ORF35464c (SEQ ID NO:389), ORF35289 (SEQ ID NO:391), ORF35410 (SEQ ID NO:393), ORF35907c (SEQ ID NO:395), ORF35534 (SEQ ID NO:397), ORF35930 (SEQ ID NO:399), ORF36246 (SEQ ID NO:401), ORF26640c (SEQ ID NO:403), ORF36769 (SEQ ID NO:405), ORF37932c (SEQ ID NO:407), ORF38640c (SEQ ID NO:409), ORF39309c (SEQ ID NO:411), ORF38768 (SEQ ID NO:413), ORF40047c (SEQ ID NO:415), ORF40560c (SEQ ID NO:417), ORF40238 (SEQ ID NO:419), ORF40329 (SEQ ID NO:421), ORF40709c (SEQ ID NO:423), ORF40507 (SEQ

ID NO:425), ORF41275c (SEQ ID NO:427), ORF42234c (SEQ ID NO:429), ORF41764c (SEQ ID NO:431), ORF41284 (SEQ ID NO:433), ORF41598 (SEQ ID NO:435), ORF42172c (SEQ ID NO:437), and ORF42233c (SEQ ID NO:152).

Replace the paragraph on page 17, lines 22-25, of the specification with the following paragraph that has been re-written in clean form.

Figs. 6B-U show the nucleotide sequences of several ORFs1-10 (SEQ ID NOS:189, 190, 191, 192, 193, 194, 195, 196, 197, and 198) identified in the 33A9 sequence and their respective amino acid sequences (ORFs1-10; SEQ ID NOS:199, 200, 201, 202, 203, 204, 205, 206, 207, and 208).

Please replace the paragraph on page 17, line 26 through page 18, line 3 of the specification with the following paragraph that has been re-written in clean form.

Fig. 7A shows the physical map of the 34B12 EcoR1 fragment map identifying the positions of three ORFs: ORF1 (L-S), ORF2, and ORF 1S. **Figs. 7B-7E** show the nucleotide sequence corresponding to the *pho34B12* insertion (SEQ ID NO:104) containing ORF1 (L-S) (SEQ ID NOS:105 and 107), ORF2 (SEQ ID NOS:106 and 108), and ORF1-S (SEQ ID NOS:159 and 209). **Figs. 7F, 7H, and 7J**, show the nucleotide sequences of ORF1 (L-S) (SEQ ID NO:105), ORF2 (SEQ ID NO:106), and ORF1-S (SEQ ID NO:159), respectively. **Figs. 7G, 7I, and 7K** show the protein sequences of ORF1 (L-S) (SEQ ID NO:107), ORF2 (SEQ ID NO: 108), and ORF1-S (SEQ ID NO: 209), respectively.

Replace the paragraph on page 18, lines 4 and 5, of the specification with the following paragraph that has been re-written in clean form.

Fig. 8 shows the deduced amino acid sequence of ORF1(L-S) (SEQ ID NO:107) which is depicted in Fig. 7G.

Replace the paragraph on page 18, lines 6 and 7, of the specification with the following paragraph that has been re-written in clean form.

Fig. 9 shows the deduced amino acid sequence of ORF2 (SEQ ID NO:108) which is depicted in Fig. 7I.

Replace the paragraph on page 18, lines 14 and 15, of the specification with the following paragraph that has been re-written in clean form.

Figs. 12A-C show the nucleotide sequence (SEQ ID NO:111) of contig 2507 identified using 36A4 nucleotide sequence.

Replace the paragraph on page 18, lines 23-25, of the specification with the following paragraph that has been re-written in clean form.

Fig. 14B shows the nucleotide sequence (SEQ ID NO:148), and **Figs. 14C** and **14D** show the predicted partial amino acid sequences of PA14 *mexA* and *mexB* (SEQ ID NOS: 149 and 150, respectively).

Replace the paragraph on page 19, lines 15 and 16, of the specification with the following paragraph that has been re-written in clean form.

Fig. 18E and **18F** show the nucleotide sequence (SEQ ID NO:164) and predicted partial amino acid sequence (SEQ ID NO:165) of PA14 *phzR,* respectively.

Replace the six paragraphs on page 19, line 27 through page 20, line 13 of the specification with the following paragraphs that have been re-written in clean form.

Figs. 24A-F show the nucleotide sequences (SEQ ID NOS:123, 124, 125, 126, 127, and 128) of the 41A5, 50E12, 35A9, pho23, 16G12, and 25F1 Tn*phoA* sequence tags, respectively.

Fig. 24G shows the nucleotide sequence (SEQ ID NO:166) and predicted

amino acid sequence (SEQ ID NO:167) of PA14 *pho15*.

Figs. 24H and 24I show the nucleotide sequence (SEQ ID NO:168) of PA14 50E12 encoding $YgdP_{Pa}$ (SEQ ID NO:169) and $PtsP_{Pa}$ (SEQ ID NO:170).

Fig. 24J shows the nucleotide sequence (SEQ ID NO:171) of PA14 35A9 encoding $mtrR_{Pa}$ (SEQ ID NO:172).

Figs. 24K and 24L show the nucleotide sequence (SEQ ID NO:173) of PA14 25F1 encoding ORFT (SEQ ID NO:174), ORFU (SEQ ID NO:175), and $DjlA_{Pa}$ (SEQ ID NO:176).

Figs. 25A and 25B show the nucleotide sequence (SEQ ID NO:129) of the *phnA* and *phnB* genes of *Pseudomonas aeruginosa* of PAO1 and PA14.

Replace the paragraph on page 20, line 25 through page 21, line 2 of the specification with the following paragraph that has been re-written in clean form.

Fig. 32A shows the physical map of the 1344 (SEQ ID NO:136) contig identified using 33C7 which illustrates three identified ORFs: ORFA (SEQ ID NO:153), ORFB (SEQ ID NO:154), and ORFC (SEQ ID NO:155). **Figs. 32B and 32C** show the nucleotide sequence of 1344 (SEQ ID NO:136). **Figs. 32D**, **32F**, and **32H** show the nucleotide sequence of ORFA (SEQ ID NO:153), ORFB (SEQ ID NO:154), and ORFC (SEQ ID NO:155), respectively. The amino acid sequences of ORFA (SEQ ID NO:156), ORFB (SEQ ID NO:157), and ORFC (SEQ ID NO:158) encoded by their respective ORFs are shown in **Figs. 32E**, **32G**, and **32I**, respectively.

Replace the paragraph on page 30, lines 1-21, of the specification with the following paragraph that has been re-written in clean form.

The nine Tn*phoA* mutants were further tested by measuring their growth rate over the course of four days in *Arabidopsis* leaves as a quantitative measure of pathogenicity (Rahme et al., *Science* 268:1899-1902, 1995; Dong et al., *Plant Cell* 3:61-72, 1991). Although none of the mutants showed any significant differences in their growth rates as compared to the wild-type strain in both rich and minimal media, the growth rate over time of all nine mutants in *Arabidopsis* leaves was lower than the wild- type strain. Table 1 lists the maximal levels of growth reached by each mutant at the fourth day post-infection. In the case of all nine mutants, less severe symptom development reflected reduced bacterial counts in leaves. All of the mutants except *33C7* elicited either weak or moderate rot and water soaking symptoms with varying amounts of chlorosis (yellowing)

(Table 1). Interestingly, however, as summarized in Table 1, the levels of proliferation of the individual mutants did not directly correlate with the severity of symptoms that they elicited. For example, even though mutant *25A12* (Fig. 21) grew to similar levels as mutants *33A9* (Figs. 5 and 6A-U), *pho34B12* (Figs. 7A-K, 8, and 9), and *34H4* (Fig. 19), and only ten-fold less than wild-type UCBPP-PA14, mutant *25A12* elicited very weak symptoms. Similarly, mutants *33C7* (Fig. 20), *pho15* (Fig. 24G), and *25F1* (Fig. 24F) all reached similar maximal levels of growth (approximately 10^3-fold less than the growth of the wild type); however, only mutant *33C7* failed to cause any disease symptoms (Table 1). The differences observed in the degree of symptoms and proliferation levels among the ten mutants suggested that these mutants likely carried insertions in genes that are involved in various stages of the plant infectious process.

Replace the paragraph on page 30, line 22 through page 31, line 2 of the specification with the following paragraph that have been re-written in clean form.

The pathogenicity of each of the nine Tn*phoA*-generated mutants that were less pathogenic in the plant leaf assay was measured in a full-thickness skin thermal burn mouse model (Rahme et al., *Science* 268:1899-1902, 1995; Stevens et al., *J. of Burn Care and Rehabil.* 15:232-235, 1994). As shown in Table 1, all nine mutants were significantly different from the wild-type with a $P \leq 0.05$ at both doses except for *25A12* and *16G12* (Fig. 24E), which were not significantly different from wild-type at the higher dose of 5×10^5 cells. In addition to the data shown in Table 1, mutant *33A9* also caused no mortality even at a higher dose of 5×10^6.

Replace the paragraph on page 35, line 24 through page 36, line 11 of the specification with the following paragraph that has been re-written in clean form.

To determine which of the ORFs encoded in the *pho34B12* region were functional, additional complementation analysis was carried out using plasmids that contained PCR products corresponding to ORF1-S, ORF1-L, and ORF2 (Figs. 7F, 7H, and 7J). The production of both pyocyanin and elastolytic activity was restored to 20-40% of wild type levels by the plasmid synthesizing the protein encoded by ORF2 (pRRLE2). Similarly, the hemolytic ability of this complemented strain was partially restored. Complementation of *pho34B12* with plasmids pRRLE1 and PRRLE15, corresponding to ORF1-S and ORF1-L, respectively, also restored the hemolytic, pyocyanin, and elastolytic activities.

Interestingly, however, the presence of plasmids pRRLE1 and pRRLE15 resulted in a 10-fold higher production of pyocyanin and a 2-fold higher level of elastase activity. Neither pRRLE1, pRRLE15, nor pRRLE2 complemented the loss of pathogenicity phenotypes of mutant *pho34B12* in either plants or animals (Table 2). Further characterization of this region including site directed mutagenesis will further elucidate which of the three ORFs is (are) required for pathogenicity in plants and animals.

Replace the paragraph on page 38, lines 19-26, of the specification with the following paragraph that has been re-written in clean form.

The 33A9 nucleic acid sequence (Figs. 5 and 6A-U) was also identified in a cosmid clone designated BI48 (Figs. 1A-C). This cosmid was sequenced in its entirety and its nucleic acid sequence is shown in Figs. 2A-K. Using standard database analysis, the nucleotide sequences and deduced amino acid sequences of several additional open reading frames were identified (Figs. 3-1 to 3-39 and 4-1 to 4-22). A summary of this analysis is presented in Table 3. Like the sequences described above, any one of the sequences found in Figs. 3-1 to 3-39 and 4-1 to 4-22 can be used to screen for compounds (e.g., using the methods described herein) that reduce the virulence of a pathogen.

Replace the paragraph on page 39, lines 1-8, of the specification with the following paragraph that has been re-written in clean form.

The sequence obtained from the pBI48 cosmid of strain PA14 revealed that 33A9 was located approximately 5 kb upstream of a pili gene cluster (Figs. 1A-C, Table 3). This cluster contains the *pilS/pilR* genes, known to be involved in the regulation of pili formation. Moreover, the analysis of the sequence upstream of 33A9 did not show any homology with previously identified sequences suggesting the possibility that the entire region surrounding 33A9 could define a pathogenicity island. Figs. 3A72 (orf 19544), Fig. 4A72 (orf 19544), 5, 6A, and 6U show the 33A9 nucleotide sequence, as well as the identified ORFs.

Replace the paragraph on page 44, line 14 through page 45, line 3 of the specification with the following paragraph that has been re-written in clean form.

In general, those mutant strains having reduced pathogenicity in plants

included *16G12*, *25A12*, *33A9*, and *33C7*; those having reduced pathogenicity in nematodes included the *35A9, 44B1, 1G2, 8C12, and 2A8*, and those having reduced pathogenicity in plants and nematodes included *25F1*, *41A5*, *50E12*, *pho15*, *12A1*, *pho23*, *34B12*, *34H4. 3E8, 23A2, and 36A4*. Tables 4 and 5 (below) summarize the pathogenicity phenotypes of these mutant strains. Sequence analysis was carried out for each of these strains having decreased virulence due to insertional mutagenesis. The DNA sequence analyses, summarized in Tables 4 and 5, showed that both novel and known genes were identified in our screening assays. Sequences from *50E12* and *41C1* each show strong similarity to previously described open reading frames (ORFs) of unknown function in *E. coli*. Mutant *35A9* identified a *mtrR* homologue of *N. gonorrhoeae* (SwissProt P39897). Mutant 25F1 identified an operon encoding 3 proteins having identity to *orfT* of *C. tepidium*, MPK, and $DjlA_{Ec}$. Sequences from *48D9*, *35H7*, and *12A1* corresponded to the *lemA*, *gacA*, and *lasR* genes, respectively. The sequences disrupted in mutants *41A5* and *44B1* do not have significant similarity to any sequence deposited in GenBank. (The *44B1*-sequence tag is only 148 bp because and there were no sequences corresponding to the 44B1 insertion in the PAO1 database were identified). Accordingly, these sequences identify additional virulence factors. The nucleotide and amino acid sequences obtained from these experiments are shown in Figs. 10, 11, 12A-C, 13, 14A-D, 15, 16, 16A, 16B, 17, 18A, 18B, 18C, 18D, and 18E and Figs. 22, 23, 24A-L, 25A, 25B, 26, 27, and 28.

Replace the paragraph on page 46, lines 5-17, of the specification with the following paragraph that have been re-written in clean form.

Mutant *pho15*. Disruption of the *dsbA* gene in *pho15* was found to be responsible for the nonpathogenic phenotypes. Fig. 24E shows the nucleotide sequence (SEQ ID NO:166) and predicted amino acid sequence (SEQ ID NO:167) of PA14 *pho15*. The pathogenicity defective phenotype of *pho15* in *C. elegans* was also found to be fully restored by constitutive expression of the *E. coli* $dsbA_{Ec}$ gene or the PA14 $dsbA_{Pa}$ gene in trans in the *pho15* background (Fig. 34B). For these experiments, the *E. coli* $dsbA_{Ec}$ gene was cloned into pUCP18 as follows. The PCR-amplified *E. coli dsbA* was cloned into the *KpnI* and *XbaI* sites of pBAD18 to form pCH3. This placed the *E. coli dsbA* under the *E. coli* arabinose promoter. A 700 bp KpnI/SphI fragment containing the *E. coli dsbA* was cloned into the *KpnI/SphI* sites of pUCP18, to make *pEcdsbA*, placing the *E. coli dsbA* under the constitutive E. coli *lacZ* promoter. pEcdsbA was subsequently used to transform PA14 and *pho15* to construct strains PA14(pEcdsbA) and *pho15*(pEcdsbA), respectively.

Replace the paragraph on page 48, lines 13-15, of the specification with the following paragraph that have been re-written in clean form.

Fig. 24J shows the nucleotide sequence (SEQ ID NO:173) of PA14 25F1 encoding ORFT (SEQ ID NO:174), ORFU (SEQ ID NO:175), and $DjlA_{Pa}$ (SEQ ID NO:176).

Replace the paragraph on page 48, lines 16 through page 49, line 4 of the specification with the following paragraph that have been re-written in clean form.

Mutant *50E12*. The Tn*phoA* insertion in 50E12 was inserted within codon 39 of a predicted 759 amino acid protein that is 43% identical (54% similar) to the $PtsP_{Ec}$ protein of *E. coli*. Based on sequence analysis, $ptsP_{Ec}$ is predicted to encode Enzyme INtr, a 738 amino acid protein which contains an N-terminal Nif-A domain and a C-terminal Enzyme I domain; the latter functions in the phosphoenolpyruvate-dependent phosphotransferase system. It is thought the Nif-A domain serves a signal transduction function, either directly sensing small molecule signals or receiving signals from a NifL-like protein. Either mechanism may modulate the catalytic activity of the Enzyme I domain; which in turn is suggested to phosphorylate NPr (nitrogen-related HPr) and thereby regulate transcription of RpoN-dependent operons. Immediately upstream of the PA14 $ptsP_{Pa}$ homologue is open reading frame (*orf159*) predicted to encode a 159 amino acid protein that appears to be co-transcribed with *ptsPPa*. Fig. 24H shows the nucleotide sequence (SEQ ID NO:168) of PA14 50E12 encoding $YgdP_{Pa}$ (SEQ ID NO:169) and $PtsP_{Pa}$ (SEQ ID NO:170). ORF159 is 62.3-64.8% identical to YgdP proteins of unknown function found in *H. influenzae* (GenBank Accession number Q57045) and *E. coli* (GenBank Accession number Q46930). These proteins are closely related to invasion protein A in *Helicobacter pylori* and *Bartonella bacilliformis*. *B. bacilliformis* invasion protein A (SwissProt Accession number P35640) is encoded by *ailA*, which when present together with an adjacent but independently transcribed gene, *ailB*, confers on *E. coli* the ability to invade human erythrocytes.

Replace the paragraph on page 49, lines 27 through page 50, line 6 of the specification with the following paragraph that have been re-written in clean form.

Mutant *35A9*. The Tn*phoA* insertion in *35A9* is located in a putative 210 amino acid protein (encoded by *orf210*) that is most closely related (31.5%

identity) to the *N. gonorrhoeae* MtrRNg protein, which belongs to the TetR family of helix-turn-helix containing bacterial transcription regulation proteins. ORF210 is adjacent to, and divergently transcribed from, three genes that are homologous to components of the energy dependent efflux (EDE) system in *P. aeruginosa.* Analyses of sequences from PA01 showed that together, these four genes defined a novel energy dependent efflux (EDE) system in *P. aeruginosa.* The other EDE systems in *P. aeruginosa* described previously are the *mexR*, *mexA-mexB-oprK* system, the *nfxB*, *mexC-mexD-oprJ* system and the *nfxC*, *mexE-mexF-oprN* system. Fig. 24H shows the nucleotide sequence (SEQ ID NO:171) of PA14 35A9 encoding $mtrR_{Pa}$ (SEQ ID NO:172).

Replace the paragraph on page 51, lines 4-20, of the specification with the following paragraph that has been re-written in clean form.

In addition, the sequence interrupted by the Tn*phoA* mutation in *3E8* was found to predict a protein with homology to the *phzB* gene from *Pseudomonas fluorescens*, that is part of an operon involved in the production of the secondary metabolite, phenazine (GenBank Accession number: L48616). The *phzB* gene also has a homolgue in *Psuedomonas aureofaciens*, referred to as *phzY.* (GenBank Accession number AF007801). Using the sequence tag, a cosmid (1G2503), containing this region in the *Pseudomonas aeruginosa* database was identified, that contains both the *phzA* and *phzB* genes, as well as other genes that are thought to play a role in phenazine biosynthesis, the *pcnC* and *D* genes (GenBank Accession number AF005404). Four of these strains, *34B12*, *3E8*, 23A12, and 35A9, were examined for pathogenicity in the mouse-burn assay. Surprisingly, these experiments showed that the phenazine defective strains have reduced pathogenesis, indicating that the genes interrupted by the Tn*phoA* insertions are mammalian virulence factors. The nucleotide and deduced amino acid sequences, including sequence tags, for these strains are shown in Figs. 7A-7K, 8, 9, 13, 14A-D, 15, 16A, 16B, 17, 18A-F, 22, 24A-L, and 33. In addition, Figs. 25 and 26 show the nucleotide sequence of the *phnA* and *phnB* genes of *Pseudomonas aeruginosa* and the deduced amino acid sequence of PHNA, respectively.

Replace the paragraph on page 55, lines 13-15, of the specification with the following paragraph that have been re-written in clean form.

We also note that we have identified a regulator, *phzR*, of the *phz* operon. Figs. 18E and 18F show the nucleotide sequence (SEQ ID NO:164) and predicted partial amino acid sequence (SEQ ID NO:165) of PA14 *phzR*.

Replace the paragraph on page 61, lines 2-7, of the specification with the following paragraph that has been re-written in clean form.

> Based on the nucleotide and amino acid sequences described herein (see, for example, Figs. 3-1 to 3-39, 4-1 to 4-22, 29, and 30), the isolation of additional coding sequences of virulence factors is made possible using standard strategies and techniques that are well known in the art. Any pathogenic cell can serve as the nucleic acid source for the molecular cloning of such a virulence gene, and these sequences are identified as ones encoding a protein exhibiting pathogenicity-associated structures, properties, or activities.

Replace the two paragraphs on page 61, line 8 through page 62, line 4 of the specification with the following paragraph that have been re-written in clean form.

> In one particular example of such an isolation technique, any one of the nucleotide sequences described herein may be used, together with conventional screening methods of nucleic acid hybridization screening. Such hybridization techniques and screening procedures are well known to those skilled in the art and are described, for example, in Benton and Davis (*Science* 196:180, 1977); Grunstein and Hogness (*Proc. Natl. Acad. Sci., USA* 72:3961, 1975); Ausubel et al. (*Current Protocols in Molecular Biology*, Wiley Interscience, New York, 1997); Berger and Kimmel (*supra*); and Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, New York. In one particular example, all or part of the 33A9 sequence (described herein) may be used as a probe to screen a recombinant plant DNA library for genes having sequence identity to the 33A9 gene (Figs. 5 and 6A-6U). Hybridizing sequences are detected by plaque or colony hybridization according to standard methods.
>
> Alternatively, using all or a portion of the amino acid sequence of the 33A9 polypeptide, one may readily design 33A9-specific oligonucleotide probes, including degenerate oligonucleotide probes (i.e., a mixture of all possible coding sequences for a given amino acid sequence). These oligonucleotides may be based upon the sequence of either DNA strand and any appropriate portion of the 33A9 sequence (Figs. 5 and 6A-6U; SEQ ID NOs:102 and 103, respectively) of the 33A9 protein. General methods for designing and preparing such probes are provided, for example, in Ausubel et al. (supra), and Berger and Kimmel, *Guide to Molecular Cloning Techniques*, 1987, Academic Press, New York. These oligonucleotides are useful for 33A9 gene isolation, either through their use as probes capable of hybridizing to 33A9 complementary sequences or as primers for various amplification techniques, for example, polymerase chain reaction (PCR)